Claim Amendments

1. (currently amended) A method for selecting a combination of nucleic acid sample pairs for evaluating the ability of an oligonucleotide probe to measure differential expression of genes, said method comprising:

(a)   conducting differential expression experiments using (i) nucleic acid sample pairs <u>wherein the pairs comprise different nucleic acid samples</u> and (ii) nucleic acid probes immobilized on a substrate, said probes representing a set of genes where the number of genes in the set is a portion of an expected number of genes in a sample, and

(b)   selecting a <u>combination of</u> nucleic acid sample <u>pairs</u> pair-combination in relation to the members of said combination having a maximized number of genes from the set of genes that exhibit differential expression and a minimized number of said genes <u>from the set of genes</u> that do not exhibit differential expression.

2. (currently amended) A method according to Claim 1 wherein a determination is made for each gene <u>in the set of genes</u> in step (a) whether the gene is differentially expressed and whether probes <u>representing a set of genes</u> for each gene cluster together.

3. (original) A method according to Claim 2 wherein said determination is made based on one or more parameters from said differential expression experiments.

4. (original) A method according to Claim 3 wherein said parameters are selected from the group consisting of LogRatio, LogRatio error and signal intensities.

5. (currently amended) A method according to Claim 3 wherein said parameters are (i) the probability of a combined LogRatio value being significantly different from zero for each of said probes representing a gene and (ii) the number of probes for a gene that have a probability of the combined LogRatio value being significantly different from zero above a threshold value.

6. (original) A method according to Claim 1 wherein said nucleic acid sample pairs are tissue pairs.

7. (original) A method according to Claim 1 wherein in step (a) said differential expression experiments are conducted by contacting a nucleic acid sample pair with a substrate having said nucleic acid probes immobilized thereon.

8. (original) A method according to Claim 1 wherein in step (a) said differential expression experiments are conducted by contacting each member of a nucleic acid sample pair with a separate substrate having said nucleic acid probes immobilized thereon.

9. (currently amended) A method for selecting a combination of nucleic acid sample pairs for evaluating the ability of an oligonucleotide probe to measure differential expression of genes, said method comprising:

(a) contacting each nucleic acid sample pair from a plurality of nucleic acid sample pairs with a plurality of probes for each of a predetermined number of genes to determine whether said genes exhibit differential expression wherein the nucleic acid sample pairs comprise different nucleic acid samples,

(b) determining for each gene and each of said nucleic acid sample pairs whether said gene exhibits or does not exhibit differential expression based on one or more parameters,

(c) for a gene that exhibits differential expression in step (b) for a nucleic acid sample pair, assigning a "yes" value, and for each gene that does not exhibit differential expression in step (b) for a nucleic acid sample pair, assigning a "no" value thereby collecting data,

(d) tabulating the data from step (c) for each ~~combination~~ of said nucleic acid sample pairs to be evaluated, and

(e) selecting a combination of nucleic acid sample pairs having a score based on a maximized number of "yes's" and a minimized number of "no's."

10. (original) A method according to Claim 9 wherein said parameters are selected from the group consisting of LogRatio, LogRatio error and signal intensities.

11. (original) A method according to Claim 9 wherein said nucleic acid sample pairs are tissue pairs.

Claims 12-19 (canceled).

20. (original) A method of identifying a sequence of a nucleic acid that is suitable for use as a substrate surface immobilized probe for a target nucleic acid, said method comprising evaluating the sequence using nucleic acid sample pairs selected by a method of claim 1.

21. (currently amended) A method of identifying a sequence of a nucleic acid that is suitable for use as a substrate surface immobilized probe for a target nucleic acid, said method comprising:

(a)   identifying a plurality of candidate nucleic acid probe sequences for said target nucleic acid based on at least one selection criterion;

(b)   empirically evaluating each of said candidate nucleic acid probe sequences under a plurality of different experimental sets to obtain a collection of empirical data values for each of said candidate nucleic acid probe sequences for each of said plurality of different experimental sets wherein said empirical evaluation employs a nucleic acid sample pair selected by a method according to Claim 1;

(c)   clustering said candidate nucleic acid probe sequences into one or more groups of candidate nucleic acid probe sequences based on each candidate nucleic acid probe sequence's collection of empirical data values, wherein each of said one or more groups exhibits substantially the same performance across said plurality of experimental sets;

(d)   selecting one of said one or more groups based on at least one criterion; and

(e)   choosing a candidate nucleic acid probe sequence from said selected group to as said sequence of said nucleic acid that is suitable for use as a substrate immobilized probe for said target nucleic acid.

22. (original) A method of producing an array of nucleic acids on the surface of a substrate, said method comprising:

(a)   identifying nucleic acid probes by a method according to Claim 21 and

(b)   synthesizing or depositing said nucleic acid probes identified in step (a) in an array on the surface of a substrate.

23. (original) A method of detecting the presence of a nucleic acid analyte in a sample, said method comprising:

(a)   contacting a nucleic acid array produced according to Claim 22 with said sample and

(b)   detecting the presence of binding complexes on the surface of said array to detect the presence of said analyte in said sample.

24. (original) A method comprising forwarding data representing a result obtained from a method of Claim 23.

25. (original) A method according to claim 23 wherein the data is transmitted to a remote location.

26. (original) A method comprising receiving data representing a result obtained from a method of Claim 23.

Claims 27-28 (canceled).